

[illegible][illegible]

Center code: W188
Web site: <http://www.vegnet.com>
Contact: sequencesubmissions@vegnet.com
Project information
Center project name: 15107
Center clone name: 521_M

* Note: This record contains 89 individual
sequences that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low Pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlapping relationships among clones to be detected.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.

1 960: contig of 960 bp in length
961 1060: gap of 100 bp
1061 1089: contig of 929 bp in length
1990 2089: gap of 100 bp
2090 2097: contig of 908 bp in length
2098 3097: gap of 100 bp
3098 4093: contig of 995 bp in length
4094 4163: gap of 100 bp
4164 5141: contig of 978 bp in length
5142 5241: gap of 100 bp
5242 6218: contig of 977 bp in length
6219 6318: gap of 100 bp
6319 7265: contig of 947 bp in length
7266 8295: contig of 930 bp in length
8296 8395: gap of 100 bp
8396 9388: contig of 993 bp in length
9389 9438: gap of 100 bp
9439 10400: contig of 971 bp in length
10410 10509: gap of 100 bp
10510 11433: contig of 924 bp in length
11434 11533: gap of 100 bp
11534 12457: contig of 924 bp in length
12458 12557: gap of 100 bp
12558 13490: contig of 933 bp in length
13491 13590: gap of 100 bp
13591 14554: contig of 963 bp in length
14555 14654: gap of 100 bp
14655 15592: contig of 938 bp in length
15593 15692: gap of 100 bp
15693 16618: contig of 925 bp in length
16619 16718: gap of 100 bp
16719 17688: contig of 970 bp in length
17689 17788: gap of 100 bp
17789 18754: contig of 966 bp in length
18755 18854: gap of 100 bp
18855 19812: contig of 958 bp in length
19813 19912: gap of 100 bp
19913 20879: contig of 967 bp in length
20880 20979: gap of 100 bp
20980 21900: contig of 921 bp in length
21901 22000: gap of 100 bp
22001 22921: contig of 921 bp in length
22922 23021: gap of 100 bp
23022 23938: contig of 917 bp in length
23939 24038: gap of 100 bp
24039 24984: contig of 946 bp in length
24985 25084: gap of 100 bp
25085 25993: contig of 909 bp in length
25994 26093: gap of 100 bp
26094 27062: contig of 969 bp in length
27063 27162: gap of 100 bp
27163 28113: contig of 951 bp in length
28114 28213: gap of 100 bp
28214 29179: contig of 966 bp in length

29180 29279: gap of 100 bp
29280 30227: contig of 948 bp in length
30228 30327: gap of 100 bp
30328 31267: contig of 940 bp in length
31268 31367: gap of 100 bp
31369 32312: contig of 945 bp in length
32313 32412: gap of 100 bp
32413 33378: contig of 966 bp in length
33379 33478: gap of 100 bp
33479 34399: contig of 921 bp in length
34400 34499: gap of 100 bp
34500 35433: contig of 934 bp in length
35434 35533: gap of 100 bp
35534 36481: contig of 948 bp in length
36482 36581: gap of 100 bp
36582 37492: contig of 911 bp in length
37493 37592: gap of 100 bp
37593 38533: contig of 941 bp in length
38534 38633: gap of 100 bp
38634 39579: contig of 922 bp in length
39579 40579: contig of 962 bp in length
40580 40679: gap of 100 bp
40680 41594: contig of 917 bp in length
41595 41694: gap of 100 bp
41695 42767: contig of 973 bp in length
42768 42867: gap of 100 bp
42868 43783: contig of 913 bp in length
43784 43883: gap of 100 bp
43884 44821: contig of 941 bp in length
44822 44921: gap of 100 bp
44922 45841: contig of 960 bp in length
45842 45941: gap of 100 bp
45942 46969: contig of 920 bp in length
46970 47009: gap of 100 bp
47010 47884: contig of 875 bp in length
47885 47984: gap of 100 bp
47985 48978: contig of 994 bp in length
48979 49078: gap of 100 bp
49079 50029: contig of 951 bp in length
50030 50129: gap of 100 bp
50130 51103: contig of 974 bp in length
51104 51203: gap of 100 bp
51204 52122: contig of 919 bp in length
52123 52222: gap of 100 bp
52223 53165: contig of 943 bp in length
53166 53265: gap of 100 bp
53266 54197: contig of 932 bp in length
54198 54297: gap of 100 bp
54298 55263: contig of 929 bp in length
55264 55363: gap of 100 bp
55364 56262: contig of 906 bp in length
56263 56362: gap of 100 bp
56363 57298: contig of 936 bp in length
57299 57398: gap of 100 bp
57399 58352: contig of 954 bp in length
58353 58452: gap of 100 bp
58453 59393: contig of 939 bp in length
59394 59493: gap of 100 bp
59494 60447: contig of 905 bp in length
60448 60547: gap of 100 bp
60548 61512: contig of 965 bp in length
61513 61612: gap of 100 bp
61613 62549: contig of 937 bp in length
62550 62649: gap of 100 bp
62650 63629: contig of 980 bp in length
63630 63729: gap of 100 bp
63730 64667: contig of 953 bp in length
64668 64787: gap of 100 bp
64788 65750: contig of 964 bp in length
65751 65850: gap of 100 bp
65851 66759: contig of 909 bp in length
66760 66859: gap of 100 bp

ID: 6502 ACTAAMCTA:AAACAAATATCA 6525

RESULT 14
AL592213

DEFINITION Homo sapiens chromosome 9 clone RP11 9611, *** SEQUENCING IN

PROGRESS *** in ordered pieces.

ACCESSION AL592213

VERSION AL592213.6 (1:1141900)

FEATURES

SOURCE Human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 155541)

AUTHORS Hammond S.

TITLE Direct Submission

JOURNAL Direct Submission

PUBLISHED 1997

REMARKS

REQUEST: chromosome 9

on Aug 9, 2001 this sequence version replaced 411702558.

Insert Sequence produced by Whitehead Institute/MIT Center for

Genome Research, 420 Charles Street,

Cambridge, MA 02141, USA

http://www.mit.edu

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: hamquerry@sanger.ac.uk

Project Information

Center Project name: h4941

Summary Statistics

Assembly program: VMAP4 version 4.5

Sequencing vector: pUC19

Sequencing vector: plasmid: 108752; 69% of reads

Chemistry: Dye-terminator ET-amersham; 4% of reads

Dye-terminator kit: Dye: 68% of reads

Chemistry: two-pyrophosphorom

Consensus quality: 15544 bases at least 90

Consensus quality: 15543 bases at least 90

Consensus quality: 15542 bases at least 90

Insert size: 15541; sum-of-counts

Insert size: 14481; 15.2% error; average

quality coverage: 15.4% in 920 bases; sum-of-counts

coverage: 15.5% in 920 bases; average

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

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Location/Qualifiers

1..155541

/organism "Homo sapiens"

/db_xref "taxon:9606"

/chromosome "9"

/clone "RP11-9611"

/clone_lib "RP11-11.1"

..155541

/note "assembly: fragment 5 of 18

clone_end: 806

vector_side:right"

BASE COUNT 50143 a 29768 c 28721 g 46899 t

ORIGIN

Query Match

Best Local Similarity 51.2% Seed 66

Matches 433 conservative 111 mismatches 59

DB 4174 ACTAAMCTA:AAACAAATATCA 6525

ID: 117 ACTAAMCTA:AAACAAATATCA 146
OR: 4124 ACTAAMCTA:AAACAAATATCA 4127RESULT 15
ACT14487/c

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota;

Mammalia;

Primates;

Catarrhini;

Hominoidea;

Homo.

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Web site: http://www.sanger.ac.uk

Contact: hamquerry@sanger.ac.uk

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Matches 433 conservative 111 mismatches 59

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```

GENERAL INFORMATION:
1 APPLICANT: YAN, Chuanhui et al.
2 TITLE OF INVENTION: ISOLATED HUMAN BASILIN-50 ANTIBODIES
3 TITLE OF INVENTION: HUMANIZED ANTIBODIES SPECIFIC TO HUMAN BASILIN-50
4 TITLE OF INVENTION: PROTEINS AND USES THEREOF
5 FILE REFERENCE: 01001079
6 CURRENT FILING DATE: 2000-07-29
7 NUMBER OF SEQ. ID NOS.: 5
8 SOFTWARE: FASTEST for Windows Version 4.0
9 SEQ. ID NO.: 3
10 LENGTH: 38865
11 TYPE: DNA
12 ORGANISM: HUMAN
13 OS=00-77-1-8926-1

Query Match: 19.48% Score 31.4; E= 19; Length 38865
Best Local Similarity: 40.78%; Prod. No. 25
Matches: 40; Consolides: 15; Mismatches: 51; Indels: 0; Gaps: 0

CY 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 
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Search completed: November 11, 2002, 10:40:20
Index time: 0:01:20

ADDENDUM: Arnold, Wilfrid & Peter Koo

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with efficiency. Full length cDNA of rat, Mammalian, human, and

1944 (1999)
 Protein structure web site (http://protein.ccr.bnl.gov) for
 further details

FEATURES

Source

Location/Qualifiers

1..361

/function "Mammalian"

/db_xref "taxon:6668"

/db_xref "taxon:6668"

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4400 Fifth Avenue, Pittsburgh, PA 15213, USA

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